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DN	01-FEB-1997 (TREMBLrel. 02, Created)
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	MOA GENE ENCODING MANGANESE OXIDIZING PROTEIN PRECURSOR.
GN	MOA.
OS	Leptothrix discophora.
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
OC	Leptothrix.
OX	NCBI_Taxid=89;
RN	[1]
RP	SEQUENCE OF 1-1150 FROM N.A.
RC	STRAIN-SS-1;
RC	Corstjens P.L.;
RA	Thesis (1993), Biochemistry, Leiden University, The Netherlands.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN-SS-1;
RC	Corstjens P.L.;
RA	Submitted (AUG-1993) to the EMBL/Genbank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN-SS-1;
RC	Corstjens P.L.A.M., de Vind J.P.M., Goosen T., de Vind-de Jong E.W.,
RA	Geomicrobiol. J. 14:91-108(1997).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN-SS-1;
RC	Corstjens P.L.;
RA	Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
DR	EMBL; Z25774; CA81037.1; -.
DR	Interpro; IPR001865; Ribosomal_S2.
KW	PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
FT	SIGNAL.
FT	CHAIN 1 33 POTENTIAL.
FT	CHAIN 34 1662 POTENTIAL.
SEQUENCE	1662 AA; 174292 MW; 639EE238600D9246 CRC64;

Query Match 55.3%; Score 57; DB 2; Length 1662;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 RMPWPKWPL 13
DB 490 RMPWPKWPL 500

RESULT 2

O9KFN3 PRELIMINARY; PRT; 236 AA.
AC O9KFN3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE BH0446 PROTEIN.
GN BH0446.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=8665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.*;
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001508; BAB04165.1; -.
KW Complete proteome.
SQ SEQUENCE 236 AA; 26968 MW; A0BD6DD9FE34FA9 CRC64;

Query Match 54.4%; Score 56; DB 2; Length 236;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 WWPWKWPL 14
DB 192 WWPWKWPL 200

RESULT 3

O9SNN3 PRELIMINARY; PRT; 165 AA.
AC O9SNN3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE HYPOTHETICAL PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa niponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone:PO493C11.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP000559; BAA84796.1; -.
SQ SEQUENCE 165 AA; 8282558ED22DE9 CRC64;

DB 10; Length 165;
1;
0; Indels 1; Gaps 1;

OY 5 PMPWPKW 12
DB 40 PMPWPKW 48

RESULT 4

O9FG26 PRELIMINARY; PRT; 676 AA.
AC O9FG26;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE NON-LTR RETROELEMENT REVERSE TRANSCRIPTION-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002032; BAB09815.1; -.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 676 AA; 76665 MW; ADIC1E18E46F53A CRC64;

Query Match 53.9%; Score 55.5; DB 10; Length 676;
Best Local Similarity 47.1%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

OY 2 RRPWPKW 11
DB 443 RRPWPKW 459

RESULT 5

O9BU12 PRELIMINARY; PRT; 491 AA.
AC O9BU12;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SIMILAR TO FERREDOXIN REDUCTASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002960; AA002960.1; -.
SQ SEQUENCE 491 AA; 53836 MW; 15D07E714F592C9D CRC64;

Query Match 51.9%; Score 53.5; DB 4; Length 491;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 SRPWPKW 12
DB 3 SRPWPKW 15

RESULT 6
O9LONO PRELIMINARY; PRT; 95 AA.

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AC 09JON0; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE F5D14.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Chan A.Y., Yu G., Lee J.M., Lenz C., Pham P., Sakano H.,
RA Toriumi M., Vyasakata V.S., Chin C., Chlou J., Choi E., Chung M.,
RA Gonzalez A., Homing B., Liu A., Vaysberg M., Altifi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
RA Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
RA Federpsel N.A.; Theologis A.;
RT "The sequence of BAC F5D14 from Arabidopsis thaliana chromosome 1.",
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
SO EMBL: AC007767; AAF81325.1; --
SEQUENCE 95 AA; 10624 MW; 0C33985771EB854E CRC64;

Query Match          51.5%; Score 53; DB 10; Length 95;
Best Local Similarity 29.6%; Pred. No. 3.9;
Matches      8; Conservative    2; Mismatches     3; Indels   14; Gaps    1;

QY      2 RRHWMP-----WKPLI 14
        | | | | |           | | | :
Db       59 RNMMWVPVLVTVDVGGEWMWMMWVPL 85

RESULT      7
ID 080790 PRELIMINARY; PRT: 970 AA.
AC 080790;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE REVERSE-TRANSCRIPTASE-LIKE PROTEIN.
DE t12j2.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.W., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RA "Arabidopsis thaliana chromosome II BAC t12j2 genomic sequence.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
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CC	-1- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE TRANSCRIPTASE)
DR	EMBL: AC004483; AAC26674.1; -
DR	InterPro: IPR000477; RVTse.
DR	Pfam: PF00078; rvl; 2.
KW	RNA-directed DNA polymerase.
SO	SEQUENCE 970 AA; 110578 MW; C3A514F63BF67A7 CRC64;
QY	4 WP-----WWPWKW 11
DB	739 WPTLFGMGIMWANKW 753
RESULT	8
ID	082276 PRELIMINARY; PRT; 1231 AA.
AC	082276;
DT	01-NOV-1998 (TREMblrel. 08, Created)
DT	01-NOV-1998 (TREMblrel. 08, last sequence update)
DT	01-JUN-2001 (TREMblrel. 17, last annotation update)
DE	POTATIVE REVERSE TRANSCRIPTASE.
GN	t16b12.11.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid 11; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. COLUMBIA;
RA	Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RT	Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT	"Arabidopsis thaliana chromosome II BAC T16b12 genomic sequence.";
RL	Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
CC	-1- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE TRANSCRIPTASE).
CC	EMBL: AC005311; AAC63844.1; -
DR	InterPro: IPR000477; RVTse.
DR	InterPro: IPR000169; ThiolProt_act_site.
DR	Pfam: PF00078; rvl; 1.
DR	ProSite: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW	RNA-directed DNA polymerase.
SO	SEQUENCE 1231 AA; 139476 MW; 5832FD600F342B1 CRC64;
Query Match	51.0%; Score 52.5; DB 10; Length 1231;
Best Local Similarity	46.7%; Pred. No. 45;
Matches 7; Conservative	0; Mismatches 1; Indels 7; Gaps 1;
QY	4 WP-----WWPWKW 11
DB	1000 WPTLFGMGIMWANKW 1014
RESULT	9
ID	09Y0E8 PRELIMINARY; PRT; 157 AA.
AC	09Y0E8;
DT	01-NOV-1999 (TREMblrel. 12, Created)
DT	01-NOV-1999 (TREMblrel. 12, last sequence update)
DT	01-JUN-2001 (TREMblrel. 17, last annotation update)
DE	SALIVARY GLAND SECRETION PROTEIN (FRAGMENT).
GN	SGS1 OR SGS-1 OR CG3047.
OS	Drosophila melanogaster (Fruit fly)
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;

RN SEQUENCE FROM N.A.
 RA Roth G.E., Matlier S., Bornschein H., Lehmann M., Korge G.;
 RT "Structure and regulation of the salivary gland secretion protein gene
 RL Sgs-1 of Drosophila melanogaster.";
 RL Genetics 0:0-0(1999).
 DR EMBL: AF156228; AAD43808.1; -
 DR FLYBASE: FBgn0003372; Sgs1.
 DR InterPro: IPR002965; P-rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENSN.
 FT NON_TER
 SQ SEQUENCE 157 AA: 17975 MW: 8495D86262819707 CRC64;

Query Match 50.5%; Score 52; DB 5; Length 157;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 WPWPKWP 12
 Db 114 WPWPKWP 121

RESULT 10
 Q915M4 PRELIMINARY; PRT; 301 AA.
 AC Q915M4;
 DT 01-MAR-2001 (TREMBL: 16, Created)
 DT 01-MAR-2001 (TREMBL: 16, Last sequence update)
 DT 01-JUN-2001 (TREMBL: 17, Last annotation update)
 DE HISTHEICAL PROTEIN PA0702.
 GN PA0702.
 OS Pseudomonas aeruginosa.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 CC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PA01;
 RX MEDLINE:20437337; PubMed:10964043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Gabor R.L., Goltzer S.N., Folger K.R., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lathig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004506; AAC04091.1; -
 DR InterPro: IPR001541; Sterol_desat.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 301 AA: 33816 MW: 09FC2935E490ABD7 CRC64;

Query Match 50.5%; Score 52; DB 2; Length 301;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WPWPKWP 13
 Db 97 WPWPKWP 106

RESULT 11
 Q9Y7V5 PRELIMINARY; PRT; 1245 AA.
 AC Q9Y7V5;
 DT 01-NOV-1999 (TREMBL: 12, Created)
 DT 01-NOV-1999 (TREMBL: 12, Last sequence update)
 DT 01-NOV-1999 (TREMBL: 12, Last annotation update)
 DE CANDIDOSPORE SURFACE PROTEIN.
 GN Cmpl.

OS Trichoderma harzianum.
 CC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Trichoderma.
 CC NCBI_TaxID=5544;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-ATCC 32173;
 RA Puyesky M., Benhamou N., Ponce Noyola P., Bauw G., Ziv T.,
 RA van Montagu M., Herrera Estrella A., Horvitz B.A.;
 RT "Developmental regulation of a gene encoding a multidomain
 RT candidospore surface protein of Trichoderma cml.";
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ133651; CAB40845.1; -
 SQ SEQUENCE 1245 AA: 135824 MW: 3249C749AFA0CDF8 CRC64;

Query Match 50.5%; Score 52; DB 3; Length 1245;
 Best Local Similarity 62.5%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WPWPKWP 11
 Db 1199 WPWPKWP 1206

RESULT 12
 Q40548 PRELIMINARY; PRT; 109 AA.
 ID Q40548;
 AC Q40548;
 DT 01-JAN-1998 (TREMBL: 05, Created)
 DT 01-JAN-1998 (TREMBL: 05, Last sequence update)
 DT 01-JUN-2001 (TREMBL: 17, Last annotation update)
 DE PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
 DE Nicotiana tabacum (Common tobacco).
 OS Nicotiana.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. PETITE HAVANA; TISSUE-PISTIL;
 RX MEDLINE:93005740; PubMed:1392607;
 RA Goldman S., Pezzotti M., Seurinck J., Mariani C.;
 RT "Developmental expression of tobacco pistil-specific genes encoding
 RT novel extensin-like proteins.";
 RL Plant Cell 4:1041-1051(1992).
 CC -1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL
 CC DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER
 CC DEVELOPMENT TOWARD ANTHERESIS. LEVELS GRADUALLY DECREASE AFTER
 CC POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER POLLINATION.
 DR EMBL: Z14014; CAA78392.1; -
 DR Mendel; 16906; Nicotiana; 2747; 16906.
 DR InterPro: IPR002965; P-rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENSN.
 KW structural protein; Repeat; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 109
 FT DOMAIN 81 109
 FT REPEAT 81 85
 FT REPEAT 93 97
 FT REPEAT 105 109
 FT REPEAT 109 109
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA: 12373 MW: 6A6BCFAC192AB8 CRC64;

Query Match 50.0%; Score 51.5; DB 10; Length 109;
 Best Local Similarity 43.8%; Pred. No. 6.8;
 Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 4 WPWPKWP 12
 Db 43 WPWPKWP 58

RESULT 13
ID 008195 PRELIMINARY; PRT; 196 AA.
AC 008195;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE CYSTEINE-RICH EXTENSIN-LIKE PROTEIN 2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93342083; PubMed=8341705;
RA Wu H.M., Zou J., May B., Gu O., Cheung A.Y.;
RT "A tobacco gene family for flower cell wall proteins with a proline-
rich domain and a cysteine-rich domain."
RL Proc. Natl. Acad. Sci. U.S.A. 90:6829-6833(1993).
DR EMBL: L13440; AAA34060.1; -
DR Mendel: 16902; Nicta:2747;16902.
SQ SEQUENCE 196 AA; 21913 MW; 4C44E23C5B706E30 CRC64;

Query Match 50.0%; Score 51.5; DB 10; Length 196;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

OY 4 WPW-----WPKWP 12
||| ||| |||
Db 40 WPWEIPCYLTWPPWP 55

RESULT 14
ID 008194 PRELIMINARY; PRT; 209 AA.
AC 008194;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR
(CYSTEINE-RICH EXTENSIN-LIKE PROTEIN 1).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93342083; PubMed=8341705;
RA Wu H.M., Zou J., May B., Gu O., Cheung A.Y.;
RT "A tobacco gene family for flower cell wall proteins with a proline-
rich domain and a cysteine-rich domain."
RL Proc. Natl. Acad. Sci. U.S.A. 90:6829-6833(1993).
DR EMBL: L13440; AAA34060.1; -
DR Mendel: 16902; Nicta:2747;16902.
SQ SEQUENCE 209 AA; 21913 MW; 4C44E23C5B706E30 CRC64;

FT SIGNAL 1 19
FT CHAIN 20 209
FT DOMAIN 81 126
FT REPEAT 81 85
FT REPEAT 93 97
FT REPEAT 105 109
FT REPEAT 117 121
FT REPEAT 122 126
FT CARBOHYD 146 146
SQ SEQUENCE 209 AA; 23351 MW; 12198BE2B8E08ED5 CRC64;

POTENTIAL
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN.
5 X 5 AA REPEATS OF S-P(4).

OY 4 WPW-----WPKWP 12
||| ||| |||
Db 45 WPWEIPCYLTWPPWP 60

Query Match 50.0%; Score 51.5; DB 10; Length 209;
Best Local Similarity 43.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

RESULT 15
ID 09S328 PRELIMINARY; PRT; 321 AA.
AC 09S328;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE PUTATIVE NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE.
GN ATG622350.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana."
RL Nature 402:761-768(1999).
DR EMBL: AC006592; AAD22368.1; -
DR RNA-directed DNA polymerase.
SQ SEQUENCE 321 AA; 36192 MW; 43736712301D41BA CRC64;

Query Match 50.0%; Score 51.5; DB 10; Length 321;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

OY 4 WPW-----WPKWP 11
||| ||| |||
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Search completed: January 30, 2002, 11:51:58
Job time: 197 sec

